



0360-2-1  
Box/SEL

THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Applicant:

Porat Erlich

Serial No.: 09/820,629

Filed: March 30, 2001

For: METHOD AND SYSTEM FOR EVALUATION  
OF ELECTRICAL CONDUCTIVITY  
OF DNA SEQUENCES

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Group Art Unit: 2857

Attorney  
Docket: 2164/4

Initial Patent Examination Division  
Commissioner of Patents and Trademarks  
Washington, D.C. 20231

CORRECTION OF APPLICATION PAPERS

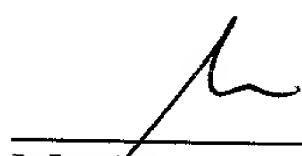
Sir:

This is in response to the Notice to File Corrected Application Papers mailed May 2, 2001, which response is being made on or before July 2, 2001, and for which no extension fees are due.

Substitute drawings in compliance with 37 CFR 1.84 are enclosed.

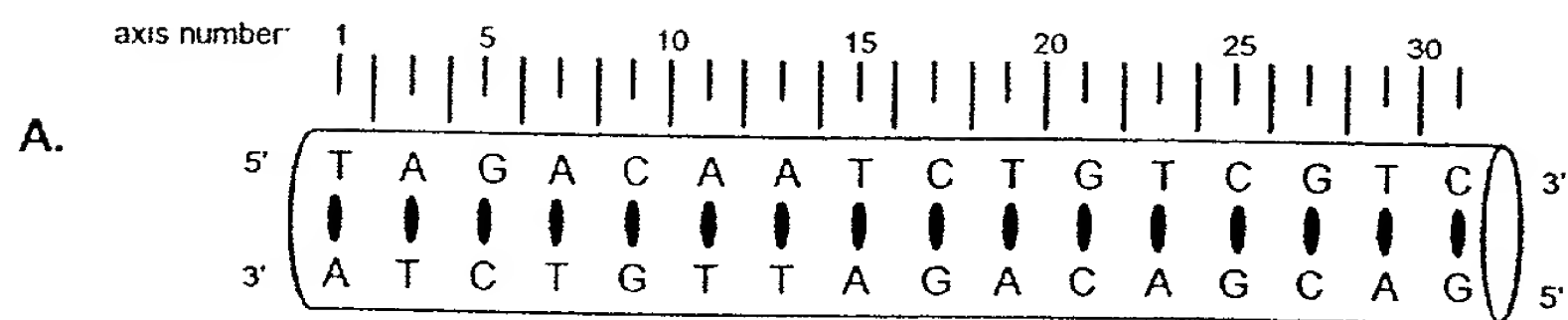
Attached is an initial paper copy of a "Sequence Listing" for the sequence presented in the current application as Figure 1A, as well as an initial computer form copy of the "Sequence Listing". Applicant respectfully requests the said "Sequence Listing" be entered into the current application. The content of the sequence listing information recorded in computer readable form is identical to the written sequence listing and includes no new matter.

Respectfully submitted,

  
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Attorney for Applicant  
Registration No. 33,883

Date: June 17, 2001

09/820,629



C.

Axis number	Polarity
10	1
11	0.4
12	1
13	0.4
14	0.8
15	0.2
16	0.8
17	0.8
18	0.6
19	0.8
20	0.8
21	0.8
22	0.8
Average	0.708

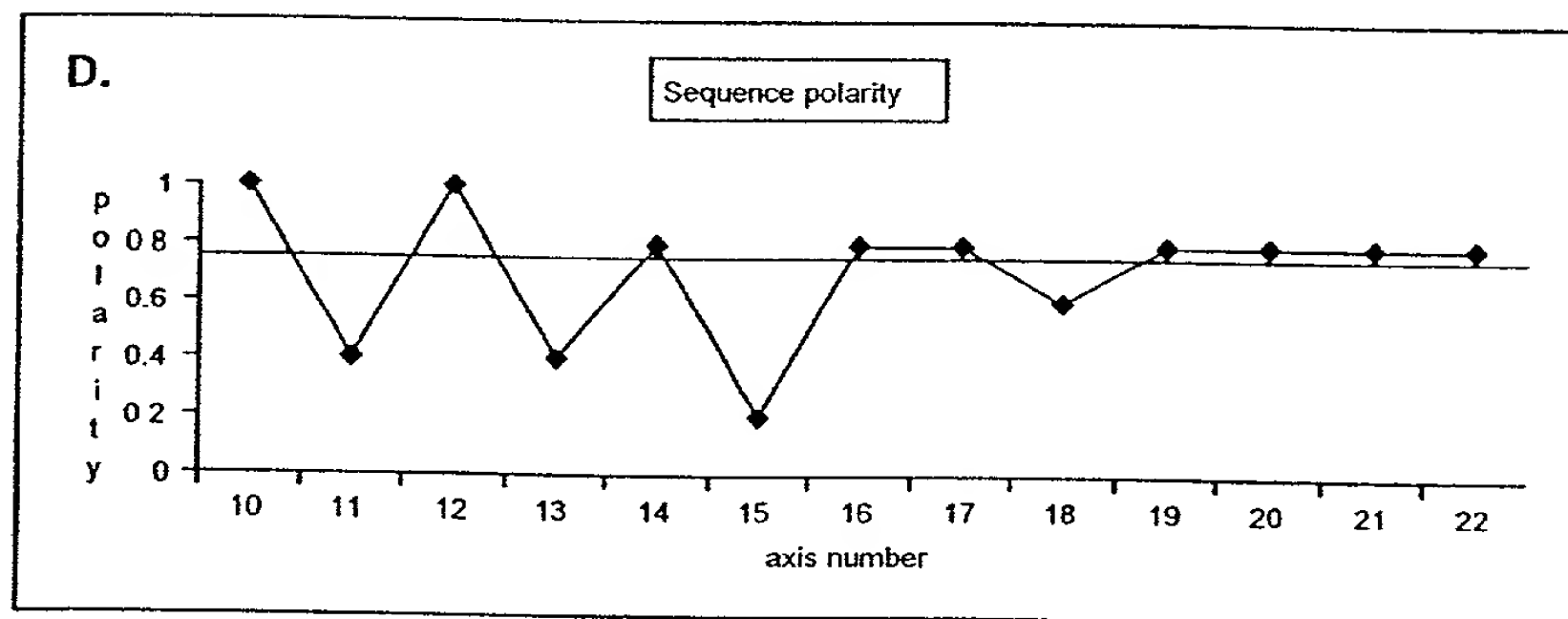
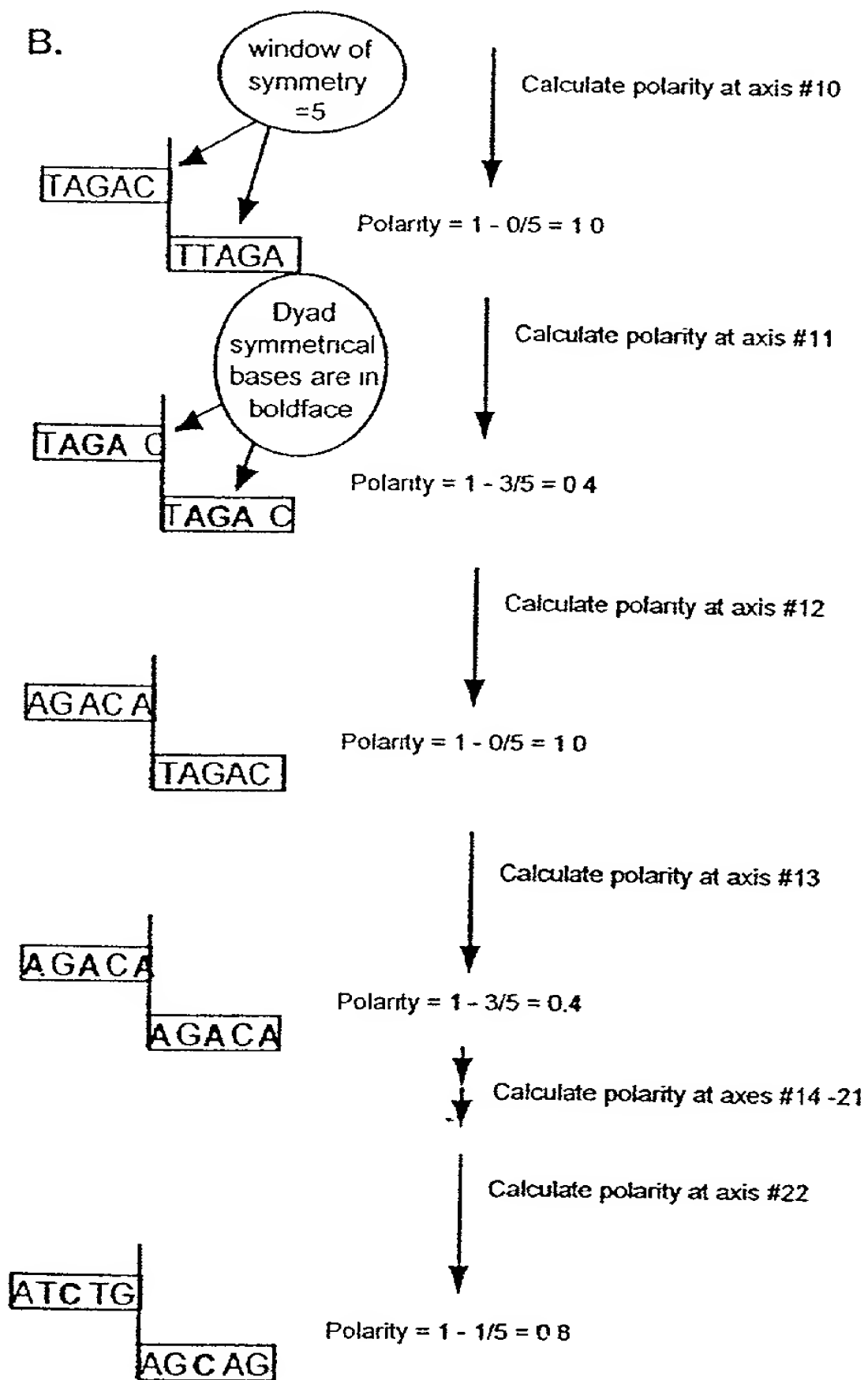
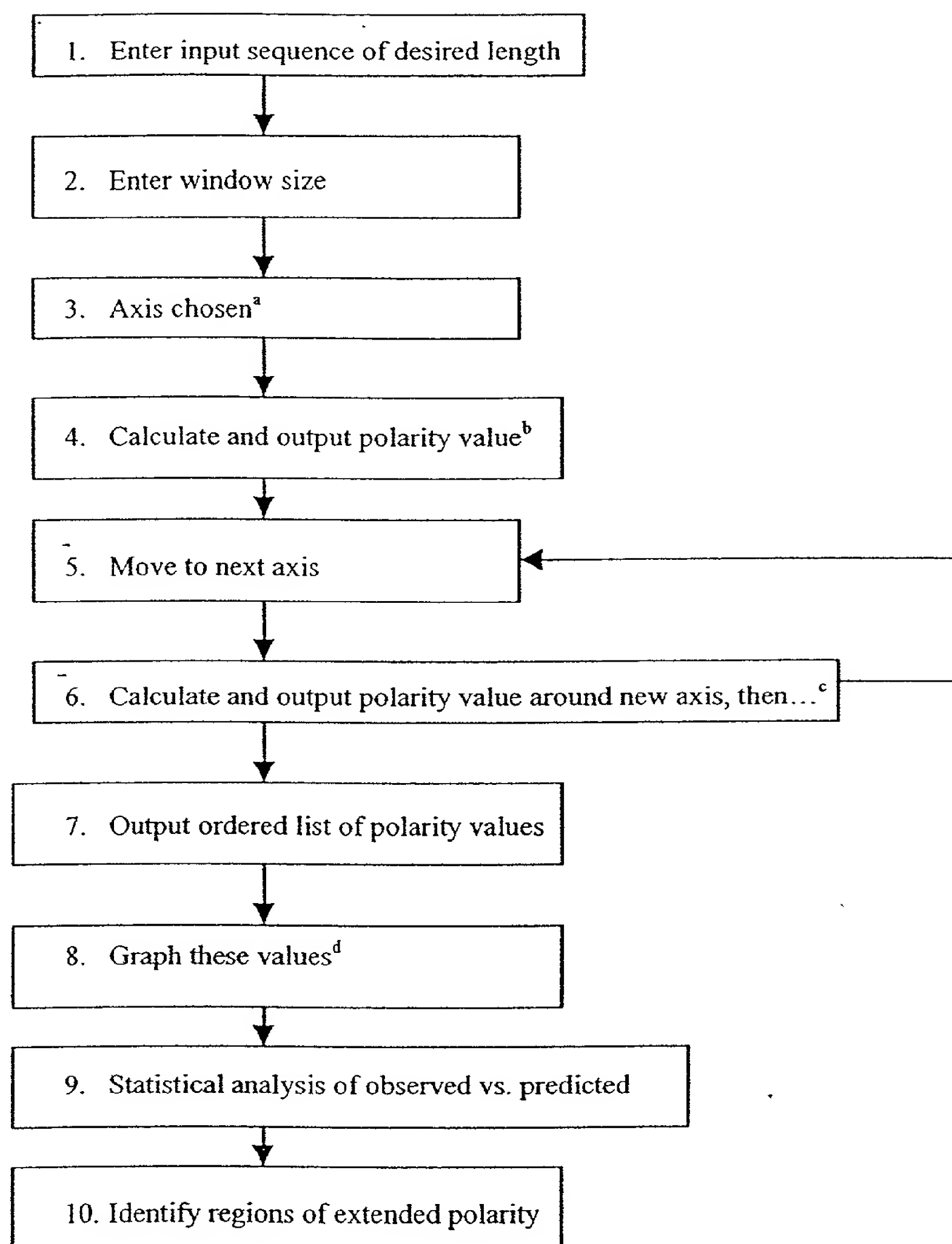


FIGURE 1





<sup>a</sup> Starting at position =  $(2 * \text{window of symmetry})$

<sup>b</sup>  $[1 - (S/W)]$

<sup>c</sup> Up to and including axis position =  $[2 * \text{length} - (2 * \text{window size})]$

<sup>d</sup> Can use a moving average of values (with number of values averaged and increment of moving being variable) to smooth curve

FIGURE 3

The algorithm was implemented in PERL programming language.  
 PERL variable-names and function-names are in boldface.

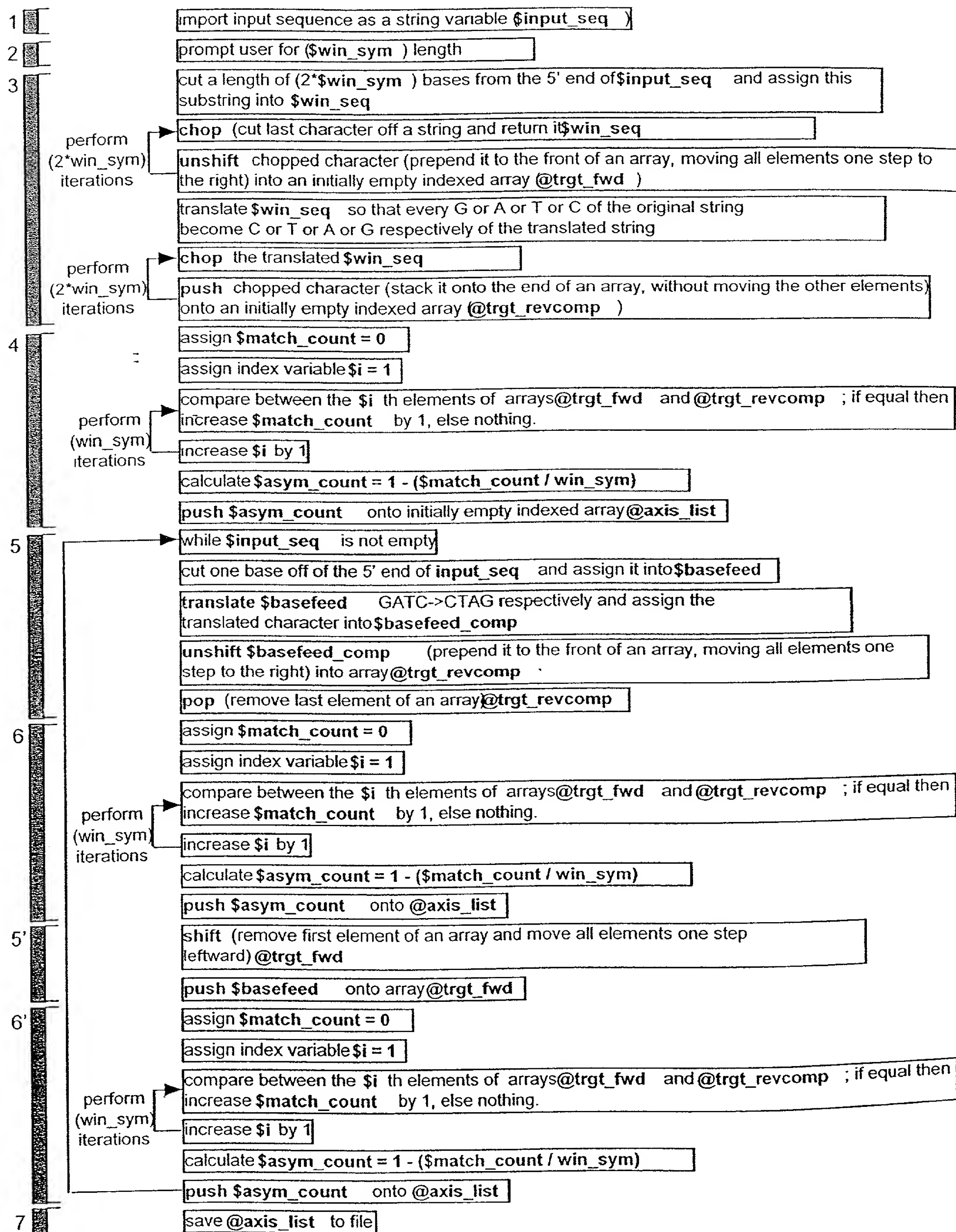
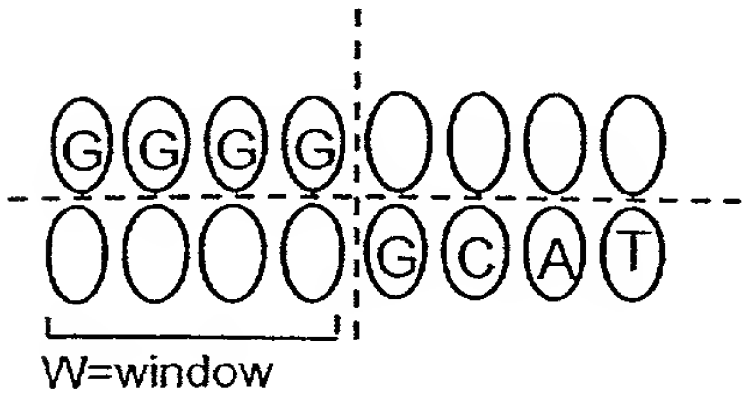


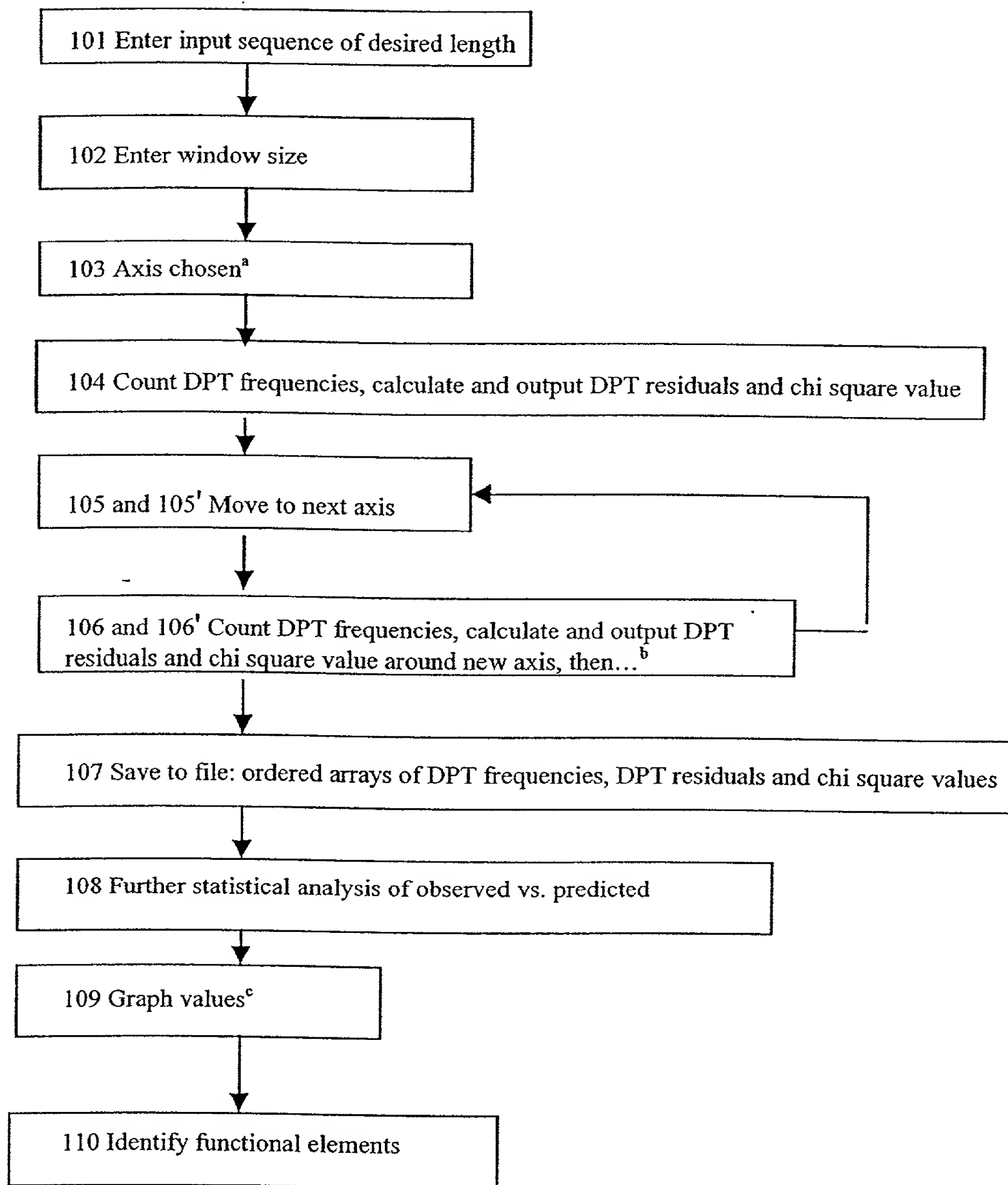
FIGURE 4

self dyad	self mirror	Purine pyrimidine dyad	Purine pyrimidine mirror
i=1: <sup>G</sup> --G	i=5: <sup>G</sup> --C	i=9: <sup>G</sup> --A	i=13: <sup>G</sup> --T
i=2: <sup>A</sup> --A	i=6: <sup>A</sup> --T	i=10: <sup>A</sup> --G	i=14: <sup>A</sup> --C
i=3: <sup>T</sup> --T	i=7: <sup>T</sup> --A	i=11: <sup>T</sup> --C	i=15: <sup>T</sup> --G
i=4: <sup>C</sup> --C	i=8: <sup>C</sup> --G	i=12: <sup>C</sup> --T	i=16: <sup>C</sup> --A

↑  
Figure 5A

Figure 5B  
↓





<sup>a</sup> Starting at axis position =  $(2 * \text{window size})$

<sup>b</sup> Up to and including axis position =  $[2 * \text{length} - (2 * \text{window size})]$

<sup>c</sup> Values include DPT frequencies, statistical measures including residuals and  $\chi^2$

FIGURE 6

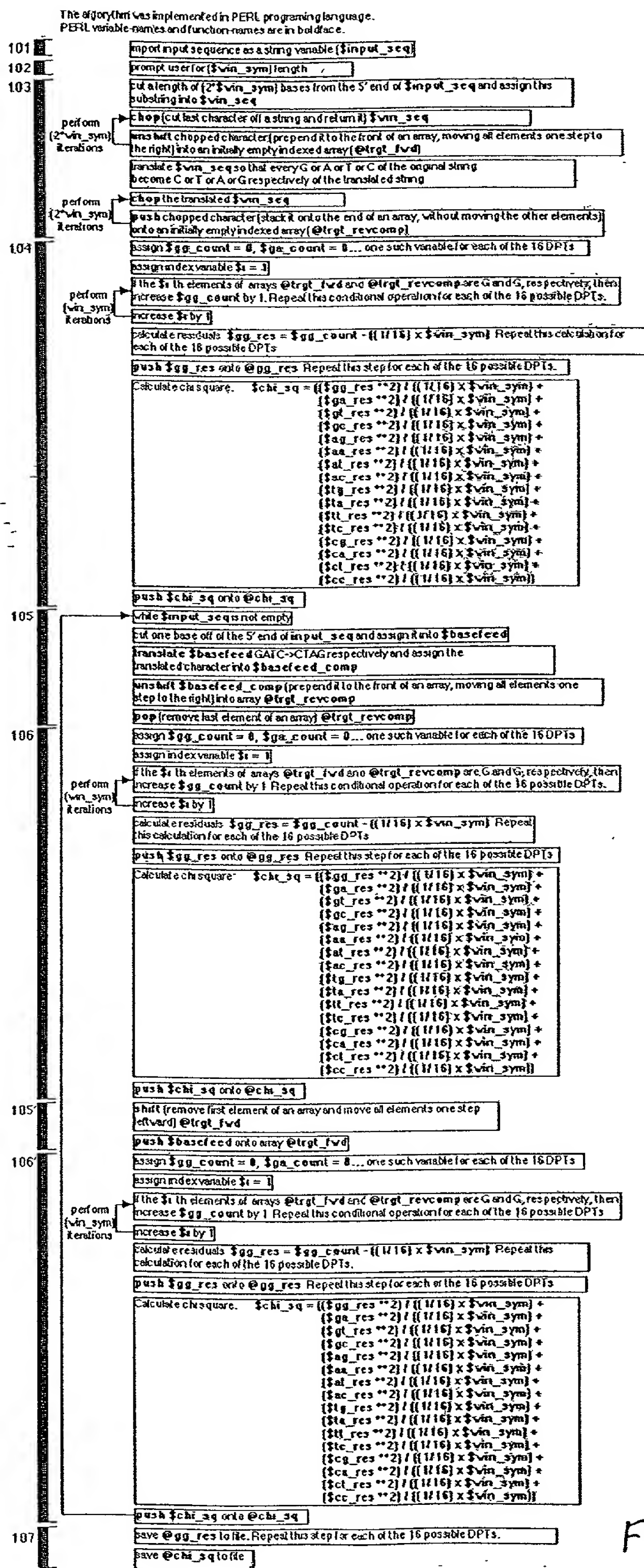


FIGURE 7



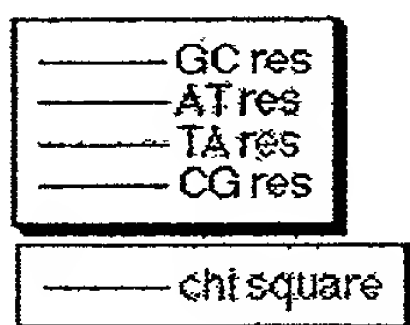
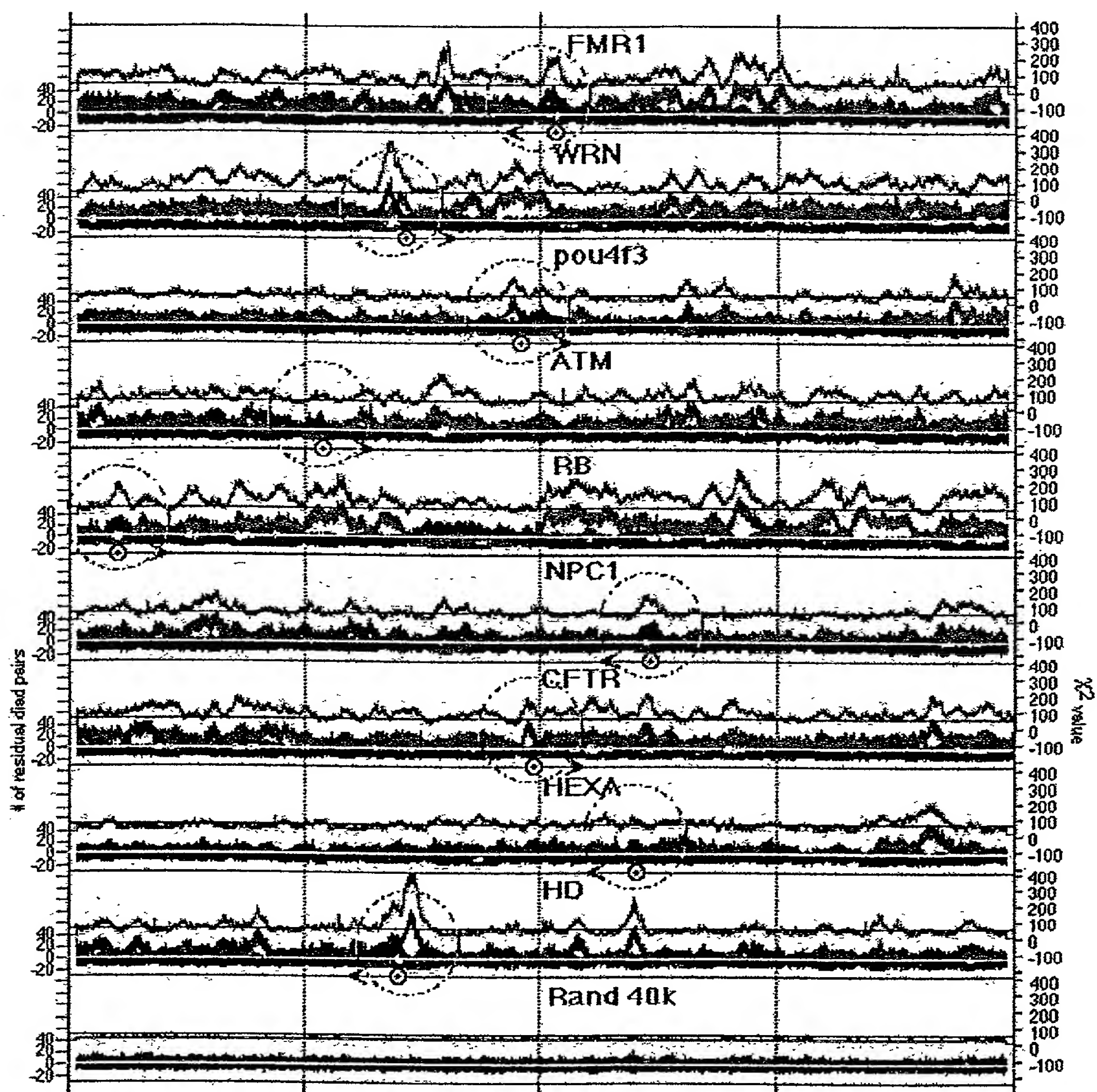


FIGURE 8



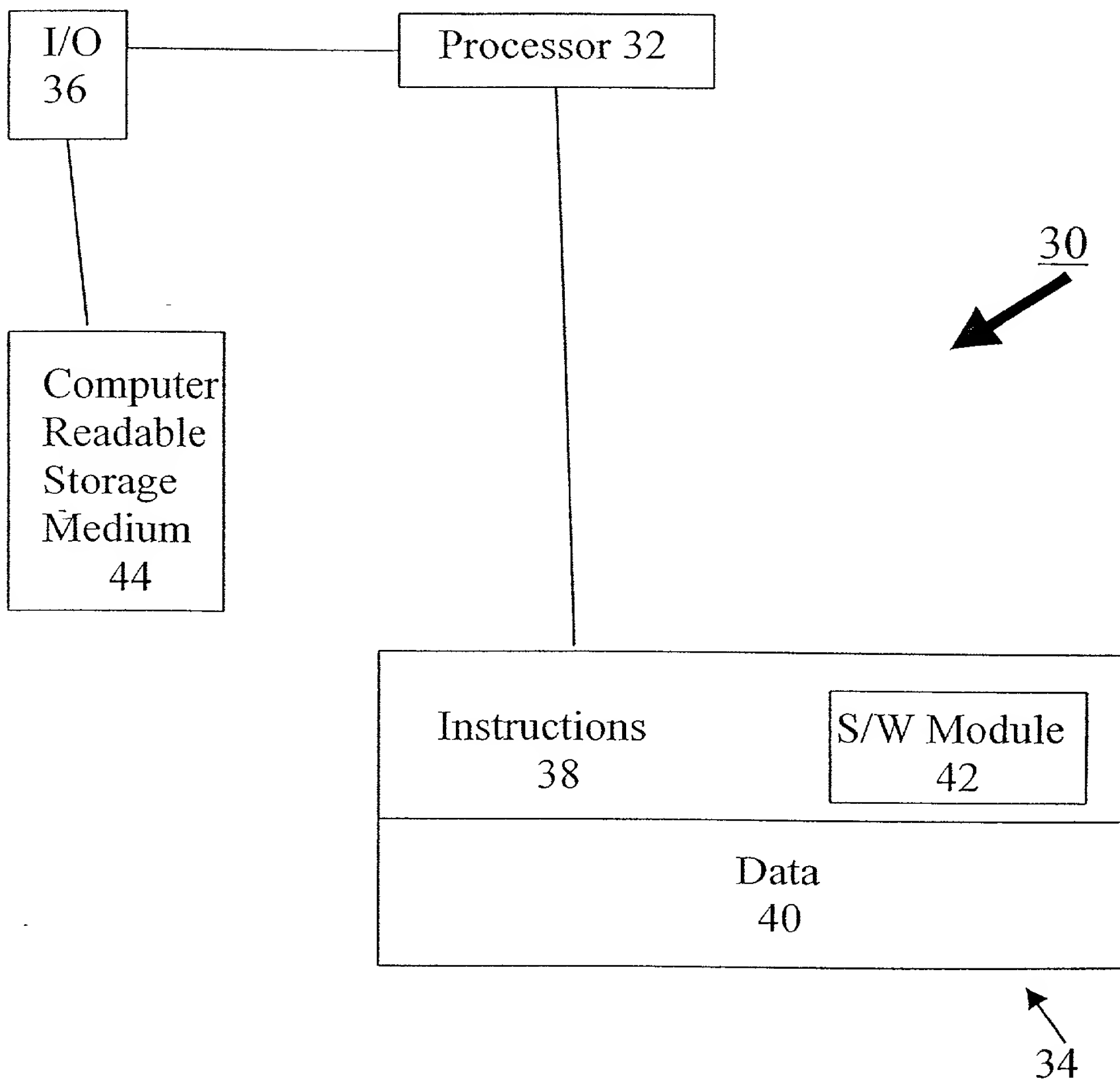


FIGURE 10